

**In the Specification:**

Please amend the specification as shown:

Please delete the paragraph on page 37, lines 3-5 and replace it with the following paragraph:

Low complexity sequence found by a filter program is substituted using the letter "N" in nucleotide sequence (e.g., "NNNNNNNNNNNNNN") (SEQ ID NO: 1) and the letter "X" in protein sequences (e.g., "XXXXXXXXXX") (SEQ ID NO: 2).

Please delete the paragraph on page 39, lines 6-16 and replace it with the following paragraph:

Five polypeptides, fragments, homologues, variants and derivatives, are typically made by recombinant means, for example as described below in the Examples. However they may also be made by synthetic means using techniques well known to skilled persons such as solid phase synthesis. The proteins may also be produced as fusion proteins, for example to aid in extraction and purification. Examples of fusion protein partners include glutathione-S-transferase (GST), 6xHis (SEQ ID NO: 488), GAL4 (DNA binding and/or transcriptional activation domains) and  $\beta$ -galactosidase. It may also be convenient to include a proteolytic cleavage site between the fusion protein partner and the protein sequence of interest to allow removal of fusion protein sequences. Preferably the fusion protein will not hinder the function of the protein of interest sequence. Proteins may also be obtained by purification of cell extracts from animal cells.

Please delete the paragraph on page 137, lines 18-26 and replace it with the following paragraph:

The DNA fragment encoding E7 of HPV type 16 is subcloned into pGEX-4T1 protein expression vector. E7 DNA fragment is amplified by polymerase chain reaction (PCR) using a set of primers: 5'-TTGTTGGATCCCATGGAGATACACCTACATTG-3' (SEQ ID NO: 3) and 5'-TTACTGAATTCTTATGGTTTCTGAGAACAGATG-3' (SEQ ID NO: 4). The amplified DNA is digested with BamH1 and EcoR1, and the resulting fragment is then cloned into the BamH1 and EcoR1 sites of pGEX- 4T1 vector. The presence of the inserted E7 is confirmed by and restriction enzyme digestion and gel electrophoresis. The accuracy of the constructs is further confirmed by DNA sequencing. The plasmid construct is transformed into Escherichia coli TG-1 for protein expression.

Please delete Appendix A on pages 160-171, and replace it with the following Appendix:

#### Appendix A: Sequences

Fve is isolated from Golden Needle Mushroom (*Flammulina velutipes*). ORGANISM: *Flammulina velutipes*. Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Agaricales; Tricholomataceae; *Flammulina*.

##### *Fve (Wild type)*

ATGTCGGCCACGTCGCTCACCTTCCAGCTTGCCTACTTGGTGAAGAAGATCGACTTCGACTACACCCC  
CAACTGGGGCCGTGGTACCCCAAGCAGCTACATCGACAACCTTACCTTCCCCAAGGTTCTCACCAGACA  
AAAAATACTCGTACCGCGTCGTGGTCAATGGCTCTGACCTTGGCGTCGAGTCCAACCTTCGCAGTGACA  
CCGTCCGGTGGGCAGACCATCAACTTCCTCCAGTACAACAAGGGGTATGGTGTGCGGGACACCAAAAC  
GATTCAAGTTTTCTGTTGTTCATTCCAGATACCGGCAACTCGGAGGAGTACATCATCGCTGAGTGAAGA  
AGACTTGA (SEQ ID NO: 5)  
msatsltfqlaylvkkidfdytpnwgrgtppssyidnltfpkvltdkkysyrvvngsdlgvesnfavt  
psggqtinlfqynkgygvadtktiqvfvpipdtgnseeyiaewkkt (SEQ ID NO: 6)  
ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/  
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/GGT/ACC/CCA/AGC/AGC/TAC/ATC/  
GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/TAC/TCG/TAC/CGC/  
GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/TTC/GCA/GTG/ACA/  
CCG/TCC/GGT/GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/AAG/GGG/TAT/GGT/  
GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/ATT/CCA/GAT/ACC/GGC/  
AAC/TCG/GAG/GAG/TAC/ATC/ATC/GCT/GAG/TGG/AAG/AAG/ACT/TGA (SEQ ID NO: 5)

A Fve (Wild type) sequence may also comprise a sequence as set out above, but lacking the initial methionine (M) in the amino acid sequence, or lacking the initial ATG in the nucleic acid sequence.

*GST-Fve (Wild type) Nucleotide Sequence*

ATGTCCCTATACTAGGTTATTGGAAAATTAAGGGCCTTGTGCAACCCACTCGACTTCTTTT  
GGAATATCTTGAAGAAAAATATGAAGAGCATTTGTATGAGCGCGATGAAGGTGATAAATGGC  
GAAACAAAAAGTTTGAATTGGGTTTGGAGTTTCCCAATCTTCCTTATTATATTGATGGTGAT  
GTTAAATTAACACAGTCTATGGCCATCATACGTTATATAGCTGACAAGCACAAACATGTTGGG  
TGGTTGTCCAAAAGAGCGTGCAGAGATTTCAATGCTTGAAGGAGCGTTTTTGGATATTAGAT  
ACGGTGTTCGAGAATTGCATATAGTAAAGACTTTGAAACTCTCAAAGTTGATTTTCTTAGC  
AAGCTACCTGAAATGCTGAAAATGTTTGAAGATCGTTTATGTCATAAAACATATTTAAATGG  
TGATCATGTAACCCATCCTGACTTCATGTTGTATGACGCTCTTGATGTTGTTTTATACATGG  
ACCAATGTGCCTGGATGCGTTCCCAAAATTAGTTTGTTTTAAAAACGTATTGAAGCTATC  
CCACAAATTGATAAGTACTTGAAATCCAGCAAGTATATAGCATGGCCTTTGCAGGGCTGGCA  
AGCCACGTTTGGTGGTGGCGACCATCCTCCAAAATCGGATCTGGAAGTTCTGTTCCAGGGGC  
CCCTGGGATCCTCCGCCACGTCGCTCACCTTCCAGCTTGCCTACTTGGTGAAGAAGATCGAC  
TTCGACTACACCCCCAACTGGGGCCGTGGTACCCCAAGCAGCTACATCGACAACCTTACCTT  
CCCCAAGGTTCTCACCGACAAAAAATACTCGTACCGCGTCGTGGTCAATGGCTCTGACCTTG  
GCGTCGAGTCCAACCTTCGCAGTGACACCGTCCGGTGGGCAGACCATCAACTTCTCCAGTAC  
AACAAGGGGTATGGTGTGCGCGACACCAAAACGATTCAAGTTTTCGTTGTCATTCCAGATAC  
CGGCAACTCGGAGGAGTACATCATCGCTGAGTGGAAGAAGACTTGA **(SEQ ID NO: 7)**

*GST-Fve (Wild type) Amino Acid Sequence*

MSPI LGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQS  
MAIIRYIADKHNMLGGCPKERAELISMLGAVLDIRYGVSR IAYSKDFETLKVDFLSKLPEMLKMFEDR  
LCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAI PQIDKYLKSSKYIAWPLQ  
GWQATFGGGDHPPKSDLEVLFGGPLGSSATSLTFQLAYLVKKIDFDYTPNWGRGTPSSYIDNLTfPKV  
LTDKKYSYRVVNGSDLGVESNFVAVTPSGGQTINFLQYNKG YGVADTKTIQVFVVIPDTGNSEYIIA  
EWKKT **(SEQ ID NO: 8)**

**FVE DELETION MUTANTS**

*Fve D6-18*

ATG/TCC/GCC/ACG/TCG/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/GGT/ACC/CCA/  
AGC/AGC/TAC/ATC/GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/  
TAC/TCG/TAC/CGC/GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/  
TTC/GCA/GTG/ACA/CCG/TCC/GGT/GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/  
AAG/GGG/TAT/GGT/GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/ATT/  
CCA/GAT/ACC/GGC/AAC/TCG/GAG/GAG/TAC/ATC/ATC/GCT/GAG/TGG/AAG/AAG/ACT/  
TGA **(SEQ ID NO: 9)**

msats/fdytpnwgrgtpssyidnltfpkvltddkysyrvvngsdlgvesnfavtpsggqtinflqy  
nkg ygvadtktiqvfvipdtgnseeyiiaewkkt **(SEQ ID NO: 10)**

*Fve D19-33*

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/  
GAC/ATC/GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/TAC/TCG/  
TAC/CGC/GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/TTC/GCA/  
GTG/ACA/CCG/TCC/GGT/GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/AAG/GGG/  
TAT/GGT/GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/ATT/CCA/GAT/  
ACC/GGC/AAC/TCG/GAG/GAG/TAC/ATC/ATC/GCT/GAG/TGG/AAG/AAG/ACT/TGA **(SEQ ID NO: 11)**

msatsltfqlaylvkkid/idnltpkvltdkkysyrvvngsdlgvesnfavtpsgggtinflqynk  
gygvadtktiqvfvpdtdgnseeyiaewkkt **(SEQ ID NO: 12)**

*Fve D34-46*

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/  
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/GGT/ACC/CCA/AGC/AGC/TAC/AAA/  
TAC/TCG/TAC/CGC/GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/  
TTC/GCA/GTG/ACA/CCG/TCC/GGT/GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/  
AAG/GGG/TAT/GGT/GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/ATT/  
CCA/GAT/ACC/GGC/AAC/TCG/GAG/GAG/TAC/ATC/ATC/GCT/GAG/TGG/AAG/AAG/ACT/  
TGA **(SEQ ID NO: 13)**

msatsltfqlaylvkkidfdytpnwgrgtpssy/kysyrvvngsdlgvesnfavtpsgggtinflqy  
nkgygvadtktiqvfvpdtdgnseeyiaewkkt **(SEQ ID NO: 14)**

*Fve D47-60*

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/  
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/GGT/ACC/CCA/AGC/AGC/TAC/ATC/  
GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/GTC/GAG/TCC/AAC/TTC/  
GCA/GTG/ACA/CCG/TCC/GGT/GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/AAG/  
GGG/TAT/GGT/GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/ATT/CCA/  
GAT/ACC/GGC/AAC/TCG/GAG/GAG/TAC/ATC/ATC/GCT/GAG/TGG/AAG/AAG/ACT/TGA  
**(SEQ ID NO: 15)**

msatsltfqlaylvkkidfdytpnwgrgtpssyidnltpkvltdk/vesnfavtpsgggtinflqyn  
kgygvadtktiqvfvpdtdgnseeyiaewkkt **(SEQ ID NO: 16)**

*Fve D61-72*

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/  
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/GGT/ACC/CCA/AGC/AGC/TAC/ATC/  
GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/TAC/TCG/TAC/CGC/  
GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/  
AAC/AAG/GGG/TAT/GGT/GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/  
ATT/CCA/GAT/ACC/GGC/AAC/TCG/GAG/GAG/TAC/ATC/ATC/GCT/GAG/TGG/AAG/AAG/  
ACT/TGA **(SEQ ID NO: 17)**

msatsltfqlaylvkkidfdytpnwgrgtpssyidnltpkvltdkkysyrvvngsdlg/qtinflq  
ynkgygvadtktiqvfvpdtdgnseeyiaewkkt **(SEQ ID NO: 18)**

*Fve D73-84*

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/  
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/GGT/ACC/CCA/AGC/AGC/TAC/ATC/  
GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/TAC/TCG/TAC/CGC/  
GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/TTC/GCA/GTG/ACA/  
CCG/TCC/GGT/GGG/GGT/GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/

ATT/CCA/GAT/ACC/GGC/AAC/TCG/GAG/GAG/TAC/ATC/ATC/GCT/GAG/TGG/AAG/AAG/  
ACT/TGA **(SEQ ID NO: 19)**  
msatsltfqlaylvkkidfdytpnwgrgtpssyidnltfpkvltdkkysyrvvvngsdlgvesnfavt  
psggg/gvadtktiqvfvipdtgnseeiyiaewkkt **(SEQ ID NO: 20)**

*Fve D85-97*

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/  
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/GGT/ACC/CCA/AGC/AGC/TAC/ATC/  
GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/TAC/TCG/TAC/CGC/  
GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/TTC/GCA/GTG/ACA/  
CCG/TCC/GGT/GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/AAG/GGG/TAT/GTC/  
ATT/CCA/GAT/ACC/GGC/AAC/TCG/GAG/GAG/TAC/ATC/ATC/GCT/GAG/TGG/AAG/AAG/  
ACT/TGA **(SEQ ID NO: 21)**  
msatsltfqlaylvkkidfdytpnwgrgtpssyidnltfpkvltdkkysyrvvvngsdlgvesnfavt  
psgggtinlfqynkgy/ipdtgnseeiyiaewkkt **(SEQ ID NO: 22)**

*Fve D98-106*

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/  
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/GGT/ACC/CCA/AGC/AGC/TAC/ATC/  
GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/TAC/TCG/TAC/CGC/  
GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/TTC/GCA/GTG/ACA/  
CCG/TCC/GGT/GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/AAG/GGG/TAT/GGT/  
GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/TAC/ATC/ATC/GCT/GAG/  
TGG/AAG/AAG/ACT/TGA **(SEQ ID NO: 23)**  
msatsltfqlaylvkkidfdytpnwgrgtpssyidnltfpkvltdkkysyrvvvngsdlgvesnfavt  
psgggtinlfqynkgygvadtktiqvfvv/yiaewkkt **(SEQ ID NO: 24)**

*Fve D107-115*

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/  
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/GGT/ACC/CCA/AGC/AGC/TAC/ATC/  
GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/TAC/TCG/TAC/CGC/  
GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/TTC/GCA/GTG/ACA/  
CCG/TCC/GGT/GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/AAG/GGG/TAT/GGT/  
GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/ATT/CCA/GAT/ACC/GGC/  
AAC/TCG/GAG/GAG/TGA **(SEQ ID NO: 25)**  
msatsltfqlaylvkkidfdytpnwgrgtpssyidnltfpkvltdkkysyrvvvngsdlgvesnfavt  
psgggtinlfqynkgygvadtktiqvfvipdtgnsee/ **(SEQ ID NO: 26)**

*Fve D61-97*

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/  
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/GGT/ACC/CCA/AGC/AGC/TAC/ATC/  
GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/TAC/TCG/TAC/CGC/  
GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/ATT/CCA/GAT/ACC/GGC/AAC/TCG/GAG/  
GAG/TAC/ATC/ATC/GCT/GAG/TGG/AAG/AAG/ACT/TGA **(SEQ ID NO: 27)**  
msatsltfqlaylvkkidfdytpnwgrgtpssyidnltfpkvltdkkysyrvvvngsdlg/ipdtgns  
eeyiaewkkt **(SEQ ID NO: 28)**

*Fve p55-100*

AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/TTC/GCA/GTG/ACA/CCG/TCC/GGT/  
GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/AAG/GGG/TAT/GGT/GTC/GCG/GAC/  
ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/ATT/CCA/GAT/ **(SEQ ID NO: 29)**  
Ngsdlgvesnfavtpsgggtinflqynkgygvadtktiqvfvipd **(SEQ ID NO: 30)**

**FVE MUTANTS WITH SINGLE AMINO ACID SUBSTITUTIONS**

*FveR27A*

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/  
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/**GCA**/GGT/ACC/CCA/AGC/AGC/TAC/ATC/  
GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/TAC/TCG/TAC/CGC/  
GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/TTC/GCA/GTG/ACA/  
CCG/TCC/GGT/GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/AAG/GGG/TAT/GGT/  
GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/ATT/CCA/GAT/ACC/GGC/  
AAC/TCG/GAG/GAG/TAC/ATC/ATC/GCT/GAG/TGG/AAG/AAG/ACT/TGA **(SEQ ID NO: 31)**  
msatsltfqlaylvkkidfdytpnwga**g**atpssyidnltfpkvltddkysyrvvngsdlgvesnfavt  
psgggtinflqynkgygvadtktiqvfvipdtgnseeyiaewkkt **(SEQ ID NO: 32)**

*FveG28A*

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/  
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/**GCA**/ACC/CCA/AGC/AGC/TAC/ATC/  
GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/TAC/TCG/TAC/CGC/  
GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/TTC/GCA/GTG/ACA/  
CCG/TCC/GGT/GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/AAG/GGG/TAT/GGT/  
GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/ATT/CCA/GAT/ACC/GGC/  
AAC/TCG/GAG/GAG/TAC/ATC/ATC/GCT/GAG/TGG/AAG/AAG/ACT/TGA **(SEQ ID NO: 33)**  
msatsltfqlaylvkkidfdytpnwgr**a**tpssyidnltfpkvltddkysyrvvngsdlgvesnfavt  
psgggtinflqynkgygvadtktiqvfvipdtgnseeyiaewkkt **(SEQ ID NO: 34)**

*FveT29A*

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/  
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/GGT/**GCA**/CCA/AGC/AGC/TAC/ATC/  
GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/TAC/TCG/TAC/CGC/  
GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/TTC/GCA/GTG/ACA/  
CCG/TCC/GGT/GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/AAG/GGG/TAT/GGT/  
GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/ATT/CCA/GAT/ACC/GGC/  
AAC/TCG/GAG/GAG/TAC/ATC/ATC/GCT/GAG/TGG/AAG/AAG/ACT/TGA **(SEQ ID NO: 35)**  
msatsltfqlaylvkkidfdytpnwgr**a**pssyidnltfpkvltddkysyrvvngsdlgvesnfavt  
psgggtinflqynkgygvadtktiqvfvipdtgnseeyiaewkkt **(SEQ ID NO: 36)**

**FUSION PROTEINS OF MAJOR HOUSE DUST MITE ALLERGEN (BLO T 5 OR DER P 2) AND FUNGAL IMMUNOMODULATORY PROTEIN FVE**

*Blo t 5-Fve (two-in-one chimeric wild type)*

caagagcacaagccaaagaaggatgatttccgaaacgaattcgatcacttggtgatcgaacaggcaaa  
ccatgctatcgaaaagggagaaacatcaattgctttacttgcaacaccaactcgacgaattgaatgaaa  
acaagagcaaggaattgcaagagaaaatcattcgagaacttgatggtggttgcgccatgatcgaagga  
gccaaggagctttggaacgtgaattgaagcgaactgatcttaacattttggaacgattcaactacga  
agaggctcaaactctcagcaagatcttgcttaaggatttgaaggaaaccgaacaaaaagtgaaggata  
ttcaaaccctaaTCCGCCACGTCGCTCACCTTCCAGCTTGCTACTTGGTGAAGAAGATCGACTTCGAC  
TACACCCCCAACTGGGGCCGTGGTACCCCAAGCAGCTACATCGACAACCTTACCTTCCCCAAGGTTCT  
CACCGACAAAAAATACTCGTACCGCGTCGTGGTCAATGGCTCTGACCTTGGCGTCGAGTCCAACCTTCG  
CAGTGACACCGTCCGGTGGGCAGACCATCAACTTCCTCCAGTACAACAAGGGGTATGGTGTGCGGGAC  
ACCAAAACGATTCAAGTTTTTCGTTGTCATTCCAGATACCGGCAACTCGGAGGAGTACATCATCGCTGA  
GTGGAAGAAGACTTGA **(SEQ ID NO: 37)**

QEHKPKKDDFRNEFDHLLIEQANHAIEKGEHQLLYLQHLDELNENKSKELQEKIIRELDVVCAMIEG  
AQGALERELKRTDLNILERFNYEEAQTLKILLKDLKETEQKVVDIQTQsatsltfqlaylvkkidfd  
ytpnwgrgtpssyidnltfpkvltddkysyrvvngsdlgvesnfavtppsggqtinflqynkgygvad  
tktiqvfvvipdtgnseeyiaewkkt **(SEQ ID NO: 38)**

*Blo t 5-FveR27A (two-in-one chimeric mutant)*

caagagcacaagccaaagaaggatgatttccgaaacgaattcgatcacttggtgatcgaacaggcaaa  
ccatgctatcgaaaagggagaaacatcaattgctttacttgcaacaccaactcgacgaattgaatgaaa  
acaagagcaaggaattgcaagagaaaatcattcgagaacttgatggtggttgcgccatgatcgaagga  
gccaaggagctttggaacgtgaattgaagcgaactgatcttaacattttggaacgattcaactacga  
agaggctcaaactctcagcaagatcttgcttaaggatttgaaggaaaccgaacaaaaagtgaaggata  
ttcaaaccctaaTCCGCCACGTCGCTCACCTTCCAGCTTGCTACTTGGTGAAGAAGATCGACTTCGAC  
TACACCCCCAACTGGGGC**GCA**GGTACCCCAAGCAGCTACATCGACAACCTTACCTTCCCCAAGGTTTC  
TCACCGACAAAAAATACTCGTACCGCGTCGTGGTCAATGGCTCTGACCTTGGCGTCGAGTCCAACCTTC  
GCAGTGACACCGTCCGGTGGGCAGACCATCAACTTCCTCCAGTACAACAAGGGGTATGGTGTGCGGGA  
CACCAAAACGATTCAAGTTTTTCGTTGTCATTCCAGATACCGGCAACTCGGAGGAGTACATCATCGCTG  
AGTGGGAAGAAGACTTGA **(SEQ ID NO: 39)**

QEHKPKKDDFRNEFDHLLIEQANHAIEKGEHQLLYLQHLDELNENKSKELQEKIIRELDVVCAMIEG  
AQGALERELKRTDLNILERFNYEEAQTLKILLKDLKETEQKVVDIQTQsatsltfqlaylvkkidfd  
ytpnwga**g**tpssyidnltfpkvltddkysyrvvngsdlgvesnfavtppsggqtinflqynkgygvad  
tktiqvfvvipdtgnseeyiaewkkt **(SEQ ID NO: 40)**

*Blo t 5-FveT29A (two-in-one chimeric mutant)*

caagagcacaagccaaagaaggatgatttccgaaacgaattcgatcacttggtgatcgaacaggcaaa  
ccatgctatcgaaaagggagaaacatcaattgctttacttgcaacaccaactcgacgaattgaatgaaa  
acaagagcaaggaattgcaagagaaaatcattcgagaacttgatggtggttgcgccatgatcgaagga  
gccaaggagctttggaacgtgaattgaagcgaactgatcttaacattttggaacgattcaactacga  
agaggctcaaactctcagcaagatcttgcttaaggatttgaaggaaaccgaacaaaaagtgaaggata  
ttcaaaccctaaTCCGCCACGTCGCTCACCTTCCAGCTTGCTACTTGGTGAAGAAGATCGACTTCGAC  
TACACCCCCAACTGGGGCCGTGGT**GCA**CCCAAGCAGCTACATCGACAACCTTACCTTCCCCAAGGTTTC  
TCACCGACAAAAAATACTCGTACCGCGTCGTGGTCAATGGCTCTGACCTTGGCGTCGAGTCCAACCTTC  
GCAGTGACACCGTCCGGTGGGCAGACCATCAACTTCCTCCAGTACAACAAGGGGTATGGTGTGCGGGA  
CACCAAAACGATTCAAGTTTTTCGTTGTCATTCCAGATACCGGCAACTCGGAGGAGTACATCATCGCTG  
AGTGGGAAGAAGACTTGA **(SEQ ID NO: 41)**

QEHKPKKDDFRNEFDHLLIEQANHAIEKGEHQLLYLQHQDELNENKSKELQEKIIRELDVVCAMIEG  
AQGALERELKRTDLNILERFNYEEAQTLSKILLKDLKETEQKVVDIQTQsatsltfqlaylvkkidfd  
ytpnwgrg**ap**ssyidnltfpkvltddkysyrvvngsdlgvesnfavtspgggtinflqynkgygvad  
tktiqvfvpdptgnseeyiaewkkt **(SEQ ID NO: 42)**

*Der p 2-FveR27A (two-in-one chimeric mutant)*

gatcaagtcgatgtcaaagattgtgccaatcatgaaatcaaaaaagttttggtaccaggatgccatgg  
ttcagaacccatgtatcattcatcggtgtaaacattccaattggaagccgttttcgaagccaacaaa  
acacaaaaacggctaaaattgaaatcaaagcctcaatcgatggtttagaagttgatgttcccggatc  
gatccaaatgcatgccattacatgaaatgccattggttaaaggacaacaatatgatattaaatatac  
atggaatgttccgaaaattgcacaaaaatctgaaaatgttgcgtcactgttaaagttatgggtgatg  
atggtgttttggcctgtgctattgctactcatgctaaaatccgcgatTCCGCCACGTCGCTCACCTTC  
CAGCTTGCCTACTTGGTGAAGAAGATCGACTTCGACTACACCCCAACTGGGGC**GCA**GGTACCCCAA  
GCAGCTACATCGACAACCTTACCTTCCCCAAGGTTCTCACCAGACAAAAAATACTCGTACCGCGTCGTG  
GTCAATGGCTCTGACCTTGGCGTCGAGTCCAACCTTCGCAGTGACACCGTCCGGTGGGCAGACCATCAA  
CTTCCTCCAGTACAACAAGGGGTATGGTGTGCGGGACACCAAAACGATTCAAGTTTTCGTTGTCTTTC  
CAGATACCGGCAACTCGGAGGAGTACATCATCGCTGAGTGGAAGAAGACTTGA **(SEQ ID NO: 43)**  
DQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEAVFEANQNTKTAKIEIKASIDGLEVDVPGI  
DPNACHYMKCPLVKGQQYDIKYTNVVPKIAPKSENVVTVKVMGDDGVLACAIATHAKIRDSatsltf  
qlaylvkkidfdytpnwgrg**ag**tpssyidnltfpkvltddkysyrvvngsdlgvesnfavtspgggtin  
flqynkgygvadtktiqvfvpdptgnseeyiaewkkt **(SEQ ID NO: 44)**

*Der p 2-FveT29A (two-in-one chimeric mutant)*

gatcaagtcgatgtcaaagattgtgccaatcatgaaatcaaaaaagttttggtaccaggatgccatgg  
ttcagaacccatgtatcattcatcggtgtaaacattccaattggaagccgttttcgaagccaacaaa  
acacaaaaacggctaaaattgaaatcaaagcctcaatcgatggtttagaagttgatgttcccggatc  
gatccaaatgcatgccattacatgaaatgccattggttaaaggacaacaatatgatattaaatatac  
atggaatgttccgaaaattgcacaaaaatctgaaaatgttgcgtcactgttaaagttatgggtgatg  
atggtgttttggcctgtgctattgctactcatgctaaaatccgcgatTCCGCCACGTCGCTCACCTTC  
CAGCTTGCCTACTTGGTGAAGAAGATCGACTTCGACTACACCCCAACTGGGGCCGTGGT**GCA**CCAA  
GCAGCTACATCGACAACCTTACCTTCCCCAAGGTTCTCACCAGACAAAAAATACTCGTACCGCGTCGTG  
GTCAATGGCTCTGACCTTGGCGTCGAGTCCAACCTTCGCAGTGACACCGTCCGGTGGGCAGACCATCAA  
CTTCCTCCAGTACAACAAGGGGTATGGTGTGCGGGACACCAAAACGATTCAAGTTTTCGTTGTCTTTC  
CAGATACCGGCAACTCGGAGGAGTACATCATCGCTGAGTGGAAGAAGACTTGA **(SEQ ID NO: 45)**  
DQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEAVFEANQNTKTAKIEIKASIDGLEVDVPGI  
DPNACHYMKCPLVKGQQYDIKYTNVVPKIAPKSENVVTVKVMGDDGVLACAIATHAKIRDSatsltf  
qlaylvkkidfdytpnwgrg**ap**ssyidnltfpkvltddkysyrvvngsdlgvesnfavtspgggtin  
flqynkgygvadtktiqvfvpdptgnseeyiaewkkt **(SEQ ID NO: 46)**

*Blo t 5-Der p 2-FveR27A (three-in-one chimeric mutant)*

caagagcacaagccaagaaggatgatttccgaaacgaattcgatcacttggtgatcgaacaggcaaa  
ccatgctatcgaaaaggagagaacatcaattgcttacttgcaacaccaactcgacgaattgaatgaaa  
acaagagcaagggaattgcaagagaaaatcattcgagaacttgatgttggtttgcgcatgatcgaagga  
gccaaggagcttgggaacgtgaattgaagcgaactgatcttaacatttgggaacgaactcaactaga  
agaggctcaaactctcagcaagatcttgcttaaggatttgaaggaaaccgaacaaaaagtggaaggata  
ttcaaaccgaagatcaagtcgatgtcaaagattgtgccaatcatgaaatcaaaaaagttttggtacca  
ggatgccatggttcagaacccatgtatcattcatcggtgtaaacattccaattggaagccgttttcga  
agccaacaaaaacacaaaaacggctaaaattgaaatcaaagcctcaatcgatggtttagaagttgatg  
ttcccggatcgatccaaatgcatgccattacatgaaatgccattggttaaaggacaacaatatgat  
attaaatatacatggaatgttccgaaaattgcacaaaaatctgaaaatgttgcgtcactgttaaagt



tatgggtgatgatggtggttttggcctgtgctattgctactcatgctaaaatccgcgatTCCGCCACGT  
CGCTCACCTTCCAGCTTGCTACTTGGTGAAGAAGATCGACTTCGACTACACCCCAACTGGGGC**GC**  
**AGGTACCCCAAGCAGCTACATCGACAACCTTACCTTCCCAAGGTTCTCACCGACAAAAATACTCGT**  
**ACCGCGTCGTGGTCAATGGCTCTGACCTTGGCGTCGAGTCCAACCTTCGCAGTGACACCGTCCGGTGGG**  
**CAGACCATCAACTTCTCCAGTACAACAAGGGGTATGGTGTGCGGACACCAAAACGATTCAAGTTTT**  
**CGTTGTCATTCCAGATACCGGCAACTCGGAGGAGTACATCATCGCTGAGTGGAAGAAGACTTGA**  
**(SEQ ID NO: 47)**  
QEHKPKKDDFRNEFDHLLIEQANHAIEKGEHQLLYLQHQLDENENKSKELQEKIIRELDVVCAMIEG  
AQGALERELKRTDLNILERFNYEEAQTL SKILLKDLKETEQKVVDIQTQDQVDVKDCANHEIKKVLVP  
GCHGSEPCIHRGKPFQLEAVFEANQNTKTAKIEIKASIDGLEVDVPGIDPNACHYMKCPLVKGQQYD  
IKYTWNVPKIAPKSENVVVTVKVMGDDGVLACAIATHAKIRDSatsltfqlaylvkkidfdytpnwga  
gtpssyidnltfpkvltddkysyrvvngsdlgvesnfavtpsgggtinflqynkgygvadtktiqvf  
vvipdtgnseeyiaewkkt **(SEQ ID NO: 48)**

## FUSION PROTEINS OF VIRAL ANTIGEN AND FVE

### HPV E7-FveT29A

MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAE PDRAHYNIVTFCKCDSTLRLC  
VQSTHVDIRTLEDLLMGTLGIVCPICSQKPsatsltfqlaylvkkidfdytpnwgrgapssyidnltf  
pkvltddkysyrvvngsdlgvesnfavtpsgggtinflqynkgygvadtktiqfvvipdtgnseey  
iaewkkt **(SEQ ID NO: 49)**  
atgcatggagatacacctacattgcatgaatatatgttagatttgcaaccagagacaactgatctcta  
ctgttatgagcaattaaatgacagctcagaggaggaggatgaaatagatggtccagctggacaagcag  
aaccggacagagcccattacaatatgttaacctttgttgcaagtgtgactctacgcttcggttggtgc  
gtacaaagcacacacgtagacattcgtactttggaagacctgttaatgggcacactaggaattgtgtg  
ccccatctgttctcagaaaccaTCCGCCACGTCGCTCACCTTCCAGCTTGCTACTTGGTGAAGAAGA  
TCGACTTCGACTACACCCCAACTGGGGCCGTGGTGCACCAAGCAGCTACATCGACAACCTTACCTTC  
CCCAAGGTTCTCACCGACAAAAATACTCGTACCGCGTCGTGGTCAATGGCTCTGACCTTGGCGTCGA  
GTCCAACCTTCGCAGTGACACCGTCCGGTGGGCAGACCATCAACTTCTCCAGTACAACAAGGGGTATG  
GTGTCGCGGACACCAAAACGATTCAAGTTTTCTGTTGTCATTCCAGATACCGGCAACTCGGAGGAGTAC  
ATCATCGCTGAGTGGAAGAAGACTTGA **(SEQ ID NO: 50)**

### HCV Core23-FveT29A

Deletion of the 23 amino acids of core antigen from 141-163 amino acid residues  
leads to increased protein production efficiency

MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKA  
RQPEGRAWAQPYPWPPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKVIDTLTCGFADLMGY  
LPLVYATGNLPGCSFSIFLLALLSCLTIPASAsatsltfqlaylvkkidfdytpnwgrgapssyidnltf  
pkvltddkysyrvvngsdlgvesnfavtpsgggtinflqynkgygvadtktiqfvvipdtgnseeyiaewkkt  
**(SEQ ID NO: 51)**  
atgagcacgaatcctaaccctcaaagaaaaaccaaacgtaaacaccaaccgcccacaggacgtcaa  
gttcccggggcggttggtcagatcggtcggtggagtttacctggtgcccgcgagggggccccaggttgggtg  
tgcgcgcgactaggaagacttccgagcggctcgcaacctcggtggaaggcgacaacctatccccaaggct  
cgccagcccaggggtagggcctgggctcagcccgggtacccctggccctctatggcaatgagggctt  
gggggtgggcaggatggctcctgtcaccccggtggtcctcggcctagttggggccccacggacccccggc

gtaggtcgcgcaatttgggtaaggtcatcgataccctcacgtgcggttcgccgatctcatgggggtac  
cttcgctcgtcggcgcaacaggggaatctgcccgggtgctccttttctatcttccttttggctttgct  
gtcctgtttgaccatcccagcttcgcttatgaagTCCGCCACGTCGCTCACCTTCCAGCTTGCCTAC  
TTGGTGAAGAAGATCGACTTCGACTACACCCCCAACTGGGGCCGTGGTGCACCAAGCAGCTACATCGA  
CAACCTTACCTTCCCCAAGGTTCTCACCACAAAAAATACTCGTACCGCGTCGTGGTCAATGGCTCTG  
ACCTTGGCGTCGAGTCCAACCTTCGCAGTGACACCGTCCGGTGGGCAGACCATCAACTTCTCCAGTAC  
AACAAAGGGGTATGGTGTGCGGGACACCAAAACGATTCAAGTTTTCGTTGTCATTCCAGATACCGGCAA  
CTCGGAGGAGTACATCATCGCTGAGTGGAAGAAGACTTGA **(SEQ ID NO: 52)**

## FUSION PROTEINS OF TUMOR-ASSOCIATED ANTIGEN AND FVE

### *MAGE3-FveT29A*

mpleqrsqhckpeegleargealglvgaqapateeeqaasssstlvevtlgevpaaesdpdpqspqga  
sslpttmnyplwsqsyedssnqeegpstfpdlesefqaalsrkvaelvfhlllkyrarepvtkaeml  
gsvvgnwqyffpvi fskassslqlvfgielmevdpighlyifatclgl sydglldnqimpkagllii  
vlaiaaregdcapeekiweelsvlevfegredsilgdpkllltqhfvgenyleyrqvpgsdpacyefl  
wgpralvetsykvvlhmvkissggphisyplhewvlregeesatsltfqlaylvkkidfdytpnwgr  
gapssyidnltfpkvltddkysyrvvngsdlgvesnfavtpsgggtinflqynkgygvadtktiqvf  
vviptdgnseeyiaewkkt **(SEQ ID NO: 53)**

atgcctcttgagcagaggagtcagcactgcaagcctgaagaaggccttgaggcccgaggagaggccct  
gggcctggtgggtgcgagggctcctgctactgaggagcaggaggtgcctcctcctcttactctag  
ttgaagtcaccctgggggaggtgctgctgccgagtcaccagatcctcccagagtcctcaggagacc  
tccagcctcccactaccatgaactaccctctctggagccaatcctatgaggactccagcaaccaaga  
agaggaggggccaagcaccttcctgacctggagtcagggtccaagcagcactcagtaggaagggtgg  
ccgagttggttcattttctgctcctcaagtatcgagccagggagccgggtcacaaaggcagaaatgctg  
gggagtgctcgtcggaattggcagtatcttcttctgtgatcttcagcaaagcttccagttccttgca  
gctggtccttggcatcgagctgatggaagtggaccccatcgccacttgtacatcttggccacctgcc  
tgggctctcctacgatggcctgctgggtgacaatcagatcatgcccaaggcaggcctcctgataatc  
gtcctggccataatcgcaagagagggcgactgtgcccctgaggagaaaatctgggaggagctgagtg  
gttagaggtgtttgaggggaggggaagacagtatcttgggggatcccaagaagctgctcaccacacatt  
tcgtgcaggaaaactacctggagtaccggcagggtccccggcagtgatcctgcatgttatgaattcctg  
tggggtccaaggggccctcggtgaaaccagctatgtgaaagtcctgcaccataggttaaagatcagtg  
aggacctcacatttcctacccacccctgcatgagtggttttgagagagggggaagagTCCGCCACGT  
CGCTCACCTTCCAGCTTGCCTACTTGGTGAAGAAGATCGACTTCGACTACACCCCCAACTGGGGCCGT  
GGTGCACCAAGCAGCTACATCGACAACCTTACCTTCCCCAAGGTTCTCACCACAAAAAATACTCGTA  
CCGCGTCGTGGTCAATGGCTCTGACCTTGGCGTCGAGTCCAACCTTCGCAGTGACACCGTCCGGTGGGC  
AGACCATCAACTTCTCCAGTACAACAAGGGGTATGGTGTGCGGGACACCAAAACGATTCAAGTTTTTC  
GTTGTCATTCCAGATACCGGCAACTCGGAGGAGTACATCATCGCTGAGTGGAAGAAGACTTGA **(SEQ ID NO: 54)**

### *MART1-FveT29A*

mpredahfiygyppkghghsyttaeeaaagigiltvilgvliligwycrrrngyralmdkslhvgtqc  
altrrcpqegfdhrdskvslqekncepvvpnapayeklsaeqspypspatsltfqlaylvkkidf  
dytpnwgrgapssyidnltfpkvltddkysyrvvngsdlgvesnfavtpsgggtinflqynkgygva  
dtktiqvfviptdgnseeyiaewkkt **(SEQ ID NO: 55)**

atgccaagagaagatgctcacttcatctatggttaccccaagaaggggcacggccactcttacaccac  
ggctgaagaggccgctgggatcggcacctgacagtgatcctgggagtccttactgctcatcggtgtt  
ggtattgtagaagacgaaatggatacagagccttgatggataaaagtcttcatgttggcactcaatgt  
gccttaacaagaagatgcccacaagaagggttgatcatcgggacagcaaagtgtctcttcaagagaa  
aaactgtgaacctgtggttcccaatgctccacctgcttatgagaaactctctgcagaacagtccacc

caccttattcacctTCCGCCACGTCGCTCACCTTCCAGCTTGCCTACTTGGTGAAGAAGATCGACTTC  
GACTACACCCCCAACTGGGGCCGTGGTGCACCAAGCAGCTACATCGACAACCTTACCTTCCCCAAGGT  
TCTCACCGACAAAAAATACTCGTACCGCGTCGTGGTCAATGGCTCTGACCTTGGCGTCGAGTCCAAC  
TCGCAGTGACACCGTCCGGTGGGCAGACCATCAACTTCTCCAGTACAACAAGGGGTATGGTGTGCGG  
GACACCAAACGATTCAAGTTTTCGTTGTTCATTCAGATACCGGCAACTCGGAGGAGTACATCATCGC  
TGAGTGGAAGAAGACTTGA (SEQ ID NO: 56)

*CEA-FveT29A*

kltiestpfnvaegkevl1lvhnlpqhlfgywykgervdgnrqiigyviggtqqatpgpaysgreiiy  
pnaslliqniiqndtgfytlhvksdlvneeatgqfrvypelpkpsissnnskpvedkdavftcepe  
tqdatylwvnnqslpvsprlqlsngnrtltlfnvtrndtasykcetqnpvsarrsdsilnvlygpd  
aptisplntsyrsgenlnlschaasnppaqyswfvngtfqgstqelfipnltvnnsgsytcqahnsdt  
glrrttvtitvyaepkpfitssnnsnpvededavaltcepeiqttylwvnnqslpvsprlqls  
nrtltllsvtrndvgpyecgignelsvdhsdpilnvlygpdptispsytyrpgvnslschaasn  
ppaqyswldigniqtqelfisniteknsglytcqannsasghsrttvktitvsaelpkpsissnns  
kpvedkdavftcepeaqttylwvnnqslpvsprlqlsngnrtltlfnvtrndarayvcgignsvs  
anrsdpvtdlvlygpdtpiispddssylsganlnlschsasnpqyswringipqghtqvlfiakit  
pnngtyacfvsnlatgrnnsivksitvsasgtspglsagatvgimigvlvgvalisatsltfqlayl  
vkkidfdytpnwgrgapssyidnltfpkvltddkysyrvvvngsdlgvesnfavtpsggqtinlfqyn  
kgygvadtktiqvfvvipdtgnseeyiiaewkkt (SEQ ID NO: 57)  
aagctcactattgaatccacgcggttcaatgtcgcagaggggaaggaggtgcttctacttgtccaaa  
tctgccccagcatcttttggctacagctggtacaaaggatgaaagagtggtggcaaccgtcaaatta  
taggatattgaataggaactcaacaagctacccagggcccgcatagtggtcgagagataatatac  
cccaatgcattccctgctgatccagaacatcatccagaatgacacaggattctacaccctacacgtcat  
aaagtcatattgtggaatgaagaagcaactggccaggttccgggtatacccgagctgccaagccct  
ccatctccagcaacaactccaaaccgtggaggacaaggatgctgtggccttcacctgtgaacctgag  
actcaggacgcaacctacctgtggtgggtaacaatcagagcctcccggtcagtcccaggctgcagct  
gtccaatggcaacaggaccctcactctattcaatgtcacaagaaatgacacagcaagctacaaatgtg  
aaaccagaacccagtgagtgcaggcgcagtgattcagtcattcctgaatgtcctctatggcccgat  
gccccaccatttcccctctaaacacatcttacagatcaggggaaaatctgaacctctcctgccatgc  
agcctctaaccacactgcacagtaactcttggtttgtcaatgggactttccagcaatccaccaagagc  
tctttatccccaacatcactgtgaataatagtggtatcctatacgtgccaagcccataactcagacact  
ggcctcaataggaccacagtcacgacgatcacagtcctatgcagagccacccaaacccttcatcaccag  
caacaactccaaccccggtggaggatgaggatgctgtagccttaacctgtgaacctgagattcagaaca  
caacctacctgtggtgggtaataatcagagcctcccggtcagtcagggtgcagctgtccaatgac  
aacaggaccctcactctactcagtggtcacaaggaatgatgtaggaccctatgagtggtgaatccagaa  
cgaattaagtgttgaccacagcgaccagtcattcctgaatgtcctctatggccagacgacccccacca  
ttccccctcatacacctattaccgtccaggggtgaacctcagcctctcctgccatgcagcctctaac  
ccacctgcacagattcttggtgattgatgggaacatccagcaacacacacaagagctctttatctc  
caacatcactgagaagaacagcggaactctatacctgccaggccaataactcagccagtggccacagca  
ggactacagtcagacaatcacagtcctctgcggagctgcccagccctccatctccagcaacaactcc  
aaaccgtggaggacaaggatgctgtggccttcacctgtgaacctgaggctcagaacacaacctacct  
gtggtgggtaaatggtcagagcctcccagtcagtcagggtgcagctgtccaatggcaacaggacc  
tactctattcaatgtcacaagaaatgacgcaagagcctatgtatgtggaatccagaactcagtgagt  
gcaaaccgcagtgaccagtcaccctggatgtcctctatgggcccggacacccccatcatttcccccc  
agactcgtcttacctttcgggagcgaacctcaacctctcctgccactcggcctctaaccatccccgc  
agtattcttggtgatcaatgggataccgcagcaacacacacaagttctctttatcgccaaaatcacg  
ccaaataataacgggacctatgcctgtttgtcttaacttggctactggccgcaataattccatagt  
caagagcatcacagtcctctgcatctggaacttctcctggtctctcagctggggccactgtcggcac  
tgattggagtgctggttgggttgctctgataTCCGCCACGTCGCTCACCTTCCAGCTTGCCTACTTG  
GTGAAGAAGATCGACTTACACCCCCAACTGGGGCCGTGGTGCACCAAGCAGCTACATCGACAA

CCTTACCTTCCCCAAGGTTCTCACCGACAAAAAATACTCGTACCGCGTCGTGGTCAATGGCTCTGACC  
TTGGCGTCGAGTCCAACCTTCGAGTGACACCGTCCGGTGGGCAGACCATCAACTTCCTCCAGTACAAC  
AAGGGGTATGGTGTGCGGGACACCAAAACGATTCAAGTTTTTCGTTGTCATTCCAGATACCGGCAACTC  
GGAGGAGTACATCATCGCTGAGTGGAAGAAGACTTGA **(SEQ ID NO: 58)**

**PRIMERS FOR CONSTRUCTION OF FIVE DELETION MUTANTS**

*Fd6-18F (36 mer)*

5' -ggA/TCC/TCC/gCC/ACg/TCg/TTC/gAC/TAC/ACC/CCC/AAC- 3' **(SEQ ID NO: 59)**

*Fd6-18R (36 mer)*

5' -gTT/ggg/ggT/gTA/gTC/gAA/CgA/CgT/ggC/ggA/ggA/TCC- 3' **(SEQ ID NO: 60)**

*Fd19-33F (36 mer)*

5' -TTg/gTg/AAg/AAg/ATC/gAC/ATC/gAC/AAC/CTT/ACC/TTC- 3' **(SEQ ID NO: 61)**

*Fd19-33R (36 mer)*

5' -gAA/ggT/AAg/gTT/gTC/gAT/gTC/gAT/CTT/CTT/CAC/CAA- 3' **(SEQ ID NO: 62)**

*Fd34-46F (36 mer)*

5' -ggT/ACC/CCA/AgC/AgC/TAC/AAA/TAC/TCg/TAC/CgC/gTC- 3' **(SEQ ID NO: 63)**

*Fd34-46R (36 mer)*

5' -gAC/gCg/gTA/CgA/gTA/TTT/gTA/gCT/gCT/Tgg/ggT/ACC- 3' **(SEQ ID NO: 64)**

*Fd47-60F (36 mer)*

5' -AAg/gTT/CTC/ACC/gAC/AAA/gTC/gAg/TCC/AAC/TTC/gCA- 3' **(SEQ ID NO: 65)**

*Fd47-60R (36 mer)*

5' -TgC/gAA/gTT/ggA/CTC/gAC/TTT/gTC/ggT/gAg/AAC/CTT- 3' **(SEQ ID NO: 66)**

*Fd61-72F (36 mer)*

5' -AAT/ggC/TCT/gAC/CTT/ggC/CAg/ACC/ATC/AAC/TTC/CTC- 3' **(SEQ ID NO: 67)**

*Fd61-72R (36 mer)*

5' -gAg/gAA/gTT/gAT/ggT/CTg/gCC/AAg/gTC/AgA/gCC/ATT- 3' **(SEQ ID NO: 68)**

*Fd73-84F (36 mer)*

5' -gTg/ACA/CCg/TCC/ggT/ggg/ggT/gTC/gCg/gAC/ACC/AAA- 3' **(SEQ ID NO: 69)**

*Fd73-84R (36 mer)*

5' -TTT/ggT/gTC/CgC/gAC/ACC/CCC/ACC/ggA/Cgg/TgT/CAC- 3' **(SEQ ID NO: 70)**

*Fd85-97F (36 mer)*

5' -CAg/TAC/AAC/AAg/ggg/TAT/ATT/CCA/gAT/ACC/ggC/AAC- 3' **(SEQ ID NO: 71)**

*Fd85-97R (36 mer)*

5' -gTT/gCC/ggT/ATC/Tgg/AAT/ATA/CCC/CTT/gTT/gTA/CTg- 3' **(SEQ ID NO: 72)**

*Fd98-106F (36 mer)*

5' -ATT/CAA/gTT/TTC/gTT/gTC/TAC/ATC/ATC/gCT/gAg/Tgg- 3' **(SEQ ID NO: 73)**

*Fd98-106R (36 mer)*

5' -CCA/CTC/AgC/gAT/gAT/gTA/gAC/AAC/gAA/AAC/TTg/AAT- 3' **(SEQ ID NO: 74)**

*Fd107-115R (39 mer)*

5' -gAT/gCA/ACT/gAA/TTC/TTA/TTA/CTC/CTC/CgA/gTT/gCC/ggT- 3' **(SEQ ID NO: 75)**

**PRIMERS FOR CONSTRUCTION OF LARGE FRAGMENT DELETION OF FVE**

*d(61-97)-F (36mer)*

5' -/AAT/ggC/TCT/gAC/CTT/ggC/ATT/CCA/gAT/ACC/ggC/AAC/- 3' **(SEQ ID NO: 76)**

*d(61-97)-R (36mer)*

5' -/gTT/gCC/ggT/ATC/Tgg/AAT/gCC/AAg/gTC/AgA/gCC/ATT/- 3' **(SEQ ID NO: 77)**

**PRIMERS FOR CONSTRUCTION OF SMALL FRAGMENT OF FVE (FROM 55AA TO 100AA)**

*[Fv55-100]-F (48mer)*

5' -  
/gTT/CCg/CgT/ggA/TCC/ATC/gAA/ggT/CgT/AAT/ggC/TCT/gAC/CTT/ggC/gTC/- 3' **(SEQ ID NO: 78)**

*[Fv55-100]-R (42mer)*

5' -/gAT/gCA/ACT/gAA/TTC/TTA/TCA/ATC/Tgg/AAT/gAC/AAC/gAA/AAC/- 3' **(SEQ ID NO: 79)**

**PRIMERS FOR CONSTRUCTION OF POINT MUTANTS OF FVE**

*F(R27A)-F (27 mer)*

5' - CCC/AAC/Tgg/ggC/gCA/ggT/ACC/CCA/AgC - 3' **(SEQ ID NO: 80)**

*F(R27A)-R (27 mer)*

5' - gCT/Tgg/ggT/ACC/TgC/gCC/CCA/gTT/ggg - 3' **(SEQ ID NO: 81)**

*F(G28A)-F (27 mer)*

5' - AAC/Tgg/ggC/CgT/gCA/ACC/CCA/AgC/AgC - 3' **(SEQ ID NO: 82)**

*F(G28A)-R (27 mer)*

5' - gCT/gCT/Tgg/ggT/TgC/ACg/gCC/CCA/gTT - 3' **(SEQ ID NO: 83)**

*F(T29A)-F (27 mer)*

5' - Tgg/ggC/CgT/ggT/gCA/CCA/AgC/AgC/TAC - 3' **(SEQ ID NO: 84)**

*F(T29A)-R (27 mer)*

5' - gTA/gCT/gCT/Tgg/TgC/ACC/ACg/gCC/CCA - 3' **(SEQ ID NO: 85)**

**PRIMERS FOR BLO T 5-FVE FUSION PROTEIN**

*Bt5Fv-F (36mer)*

5' - /AAg/gAT/ATT/CAA/ACC/CAA/TCC/gCC/ACg/TCg/CTC/ACC/-3' **(SEQ ID NO: 86)**

*Bt5Fv-R (36mer)*

5' - /ggT/gAg/CgA/CgT/ggC/ggA/TTg/ggT/TTg/AAT/ATC/CTT/-3' **(SEQ ID NO: 87)**

**PRIMERS FOR DER P 2-FVE FUSION PROTEIN**

*Dp2Fv-F (36mer)*

5' - /CAT/gCT/AAA/ATC/CgC/gAT/TCC/gCC/ACg/TCg/CTC/ACC-3' **(SEQ ID NO: 88)**

*Dp2Fv-R (36mer)*

5' - /ggT/gAg/CgA/CgT/ggC/ggA/ATC/gCg/gAT/TTT/AgC/ATg-3' **(SEQ ID NO: 89)**

**PRIMERS FOR BLO T 5-DER P 2-FVE FUSION PROTEIN**

*Bt5Dp2-F (36mer)*

5' - /aag/gat/att/caa/acc/caa/gat/caa/gtc/gat/gtc/aaa/-3' **(SEQ ID NO: 90)**

*Bt5Dp2-R (36mer)*

5' - /ttt/gac/atc/gac/ttg/atc/ttg/ggt/ttg/aat/atc/ctt/-3' **(SEQ ID NO: 91)**

Please delete the Appendix B header on page 172, and replace it with the following header:

**APPENDIX B: FVE FRAGMENTS (RGT TRIPLET HIGHLIGHTED)**

**(APPENDIX DISCLOSES SEQ ID NOS: 92-487, RESPECTIVELY, IN ORDER OF APPEARANCE.)**